Approximations to the Quasistationary Distributions of the SIS and SEIS Epidemic Models for General Distribution of the Duration of the Infectious State.

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Summary

In this paper it is shown that under certain mild conditions, good approximations to the quasistationary distribution of the Susceptible- Infected- Susceptible (SIS) and Susceptible- Latent- Infected- Susceptible (SEIS) epidemic models can be obtained using results from queuing theory, for a general distribution of the duration of the infectious state.

Keywords: *Epidemic models, quasistationary distribution, Continuous time Markov chains, SIS epidemic model, SEIS epidemic model.*

1 Introduction

In closed population stochastic epidemics models the process reaches an absorbing state once the population is free of infected individuals. Absorption into this state will occur eventually, with the time to reach this depending strongly on the

infection potential $\rho = \lambda/\mu$, therefore, the process has a degenerate limiting distribution ($t \to \infty$) with all its weight at state 0.

The expected time to extinction generally increases with ρ, thus, an interesting property of these process is its behavior before going to absorption. The idea behind the quasistationary distribution is to analize the limiting distribution of the process conditioning in this not being absorbed (see Darroch and Seneta, 1967, Cavender 1978). These distributions are difficult to find and instead some good approximations are suggested, like the "reflecting state 0" or the "one permanently infected". These distributions were in turn approximated, (see Kryscio and Lefèvre, 1989).

Altough the approximations to the quasistationary distribution of the number of infectives seems not to have a close "known" distribution, this paper proves that that of the susceptibles is Poisson distributed for general distribution of the infectious state. Since the natural next step is to add a latent period that allows for the incubation of the disease, the approach is applied to an SEIS epidemic model.

In this paper we derive the distribution of the approximation "one permanently infected", for general duration of the infection state, for SIS and SEIS models. The term *conditional endemic distribution* is used here for this type distributions. This paper is organized as follows: section 2 and 3 are devoted to the SIS and SEIS model respectively. Section 1 introduces the SIS model, section 2 and 3 introduces the quasistationary distribution for the SIS and its approximations. In section 4 the case of a general distribution of the infectious state is analyzed using standard results from queuing theory, and numerical comparisons of these results via simulations are presented in section 5. In section 3.1 the SEIS model is introduced. In section 3.2 it is shown that the quasistationary distribution of the infected individuals (latent +

infective) can be approximated with that of an SIS model with appropriate parameters. An aproximation to the quasistationary joint distribution of latent and infective is also derived in this section. A miscellaneous result conecring the time between two infections is given in section 3.3 and numerical comparisons are presented in section 3.4.

2 The SIS Model

2.1 Introduction

The susceptible-infected-susceptible (SIS) stochastic epidemic model attempt to reproduce the behavior of epidemics running through a population with no vital dynamics, that is, no births and deaths occur, and hence are quite useful to model simple outbreaks for which there is data available. It is assumed no individuals are removed from circulation either by recovery or isolation. The deterministic version of the SIS model was introduced by Kermack and McKendrick (1927) and was fully analyzed since then. Its stochastic counterpart, also called the stochastic logistic epidemic model (Norden, 1982) or stochastic simple epidemics model, was early introduced by Weiss and Dishon (1971), and has been applied similarly to study the transmission of rumors (Bartholomew, 1976), however, most of the relevant results concerning this model have been in the epidemics context.

In the SIS model, susceptible individuals may become infected by contact with infective individuals and hence it is assumed that there is no incubation period for the disease, that is, infected individuals become infectious immediately. After some time, they become healthy and susceptible again. The process of contagion is assumed to be driven by homogeneous mixing of individuals in the population.

We let $I(t)$ and $S(t)$ be the number of infectives and susceptibles at time t, and note that since the population is closed, the state of the process at time t can be fully described by either $I(t)$ or $S(t)$. It is customary o use the former.

$I(t)$ takes values on $\Omega = \{0, 1, 2, \ldots, N\}$, N being the population size. Therefore, the SIS stochastic epidemic model is a discrete space, continuous time Markov Chain. In particular, it is a unidimensional continuous time birth- death process. Upon defining

$$P_{j,k}(s,t) = P\{I(t) = k \,|\, I(s) = j\},\ j,k \in \Omega,\ 0 \leq s \leq t,$$

then the instantaneous transition rates can be written as

$$P_{k,k+1}(t, t+\delta) = \lambda\, \delta\, k(N-k)/N + o(\delta) \tag{2.1}$$

$$P_{k,k-1}(t, t+\delta) = \mu\, \delta\, k + o(\delta).$$

From the above expressions, it can be seen that the mass action law plays an important role and results from the assumption of homogeneous mixing.

One way to dissect the process given by (2.1) is by specifying the following set of rules:

i) Every individual becomes in contact with other at random intervals which are *iid.* The distribution of these intervals is exponential with parameter β. If a contact involves a susceptible and an infectious, the probability of infection is θ.

ii) The duration of the infectious state is an exponential random variable with parameter μ.

From i, all k infective individuals come in close contact with other according to a Poisson process with parameter $\beta\, k$, since every one of these contacts could be with a susceptible individual with probability $(N-k)/N$, by thinning the Poisson process, we conclude that for fixed k, contacts between infective and susceptible individuals that will end up in a infection of the susceptible occur according to a Poisson process with parameter $\beta\ \theta\ k\ (N-k)/N$. Letting $\lambda = \beta\ \theta$ yields the first equation of (2.1). The second equation follows directly from ii.

2.2 The quasi-stationary distribution

We are interested in the future of the epidemics, which depends strongly on the ratio $\rho = \lambda/\mu$, called the transmission factor, basic reproduction ratio, basic reproduction number or infection potential. The deterministic model has a threshold at $\rho = 1$, and it results in an endemic infection of size $N(1-\mu/\rho)$ if this value is greater than 1. In the stochastic model, since $\{0\}$ is an absorbing state that can be reached with positive probability, the process will end up in this state for any value of ρ given a sufficient amount of time, for any initial number of infectives. The certainty of extinction imposes a problem if our interest is in the long-time behavior of the

epidemics, that is, in finding an expression for the distribution

$$\Pi = \{\pi_0, \pi_1, \pi_2, \ldots, \pi_N\}$$

where

$$\pi_j = \lim_{t \to \infty} \frac{X_j(t)}{t},$$

$X_j(t)$ being the time spent in state j up to time t, $j \in \Omega$. Thus, π_j denotes the proportion of time spent in state j as $t \to \infty$. $\underline{\Pi}$ is called the stationary distribution of the process. If $p_j(t)$ denotes the probability that the process is in state j at time t then it is possible to give an alternative representation for π_j

$$\pi_j = \lim_{t \to \infty} p_j(t).$$

The stationary distribution for the SIS epidemic model is degenerated with all its mass in state $\{0\}$, which is true for any finite value of ρ. However when $\rho \gg 1$ it is reasonable to assume that the disease will be in an endemic state for a while, and any information on the behavior of the process previous to extinction would be useful in the understanding of the epidemics. This interest led to the development of the concept of quasi-stationary distributions.

Quasi-stationary distributions (QSD) are limiting distributions conditioning on the process not being in an absorbing state. If we let

$$Q = \{q_1, q_2, \ldots, q_N\}$$

denote the quasi-stationary distribution of the SIS epidemics thus

$$q_j = \lim_{t\to\infty} \left(p_j(t) \,\middle|\, I(t) \neq 0\right)$$

$$= \lim_{t\to\infty} \frac{p_j(t)}{1 - p_0(t)}.$$

Observe that when $\rho \gg 1$, Q is a conditional endemic state distribution. No simple expression exists to calculate Q although Nåsell (1993) proposed a numerical algorithm for its calculation. Most of the relevant work regarding the calculation of analytical expressionsQSD of the SIS model is based on approximation methods.

Two of these approximations were suggested by Kryscio and Lefèvre (1989) and analyzed in detail by Nåsell (1993). The common characteristic of these approximations is that the process is modified in such a way that it lacks the absorbing state $\{0\}$ and thus the possibility of degenerate distributions is avoided. In one approximation the number of infectives in the population is at least one and is called the SIS model with one permanently infected individual. In this process every recovery rate $\mu_j = \mu j$ is replaced by $(j-1)\mu$, while the infection rates are unchanged. In the second approximation, the only rate that is changed is μ_1, which is replaced by zero. This latter is refered as the SIS model with the origin removed or reflecting state approximation model (Nåsell, 1991). Here we use the notation where $q_j^{(1)}$ denotes the approximation to q_j when using one permanently infected individual and $q_j^{(0)}$ denotes the reflecting state approximation model.

Our aim is to analize the asymtotic behavior of the SIS when $\rho \gg 1$ and N is large. For this, it has been proved by Kryscio and Lefèvre (1989) that

$$\sum_{j=1}^{m} q_j \approx \sum_{j=1}^{m} q_j^{(0)}$$

In addition, Nåsell (1993), proved that for $\rho > 1$, the distribution of the number of infectives under both the reflecting state 0 approximation and the one with one permanently infected individual are approximately Normal with mean $N(1-\mu/\lambda)$ and variance $N\mu/\lambda$.

2.3 The approximation to the quasi-stationary distribution of the number of infectives.

In the following calculations we derive an approximation for the QSD of the infective individuals. It is surprisingly simple to derive the approximation to the QSD of the number of susceptibles instead of that of the infected. We establised a new result: that the distribution of the QSD of the number of susceptibles is well approximated by a Poisson truncated at zero.

We use the recurrence relations

$$\pi_n = \frac{\lambda_1\,\lambda_2\,\lambda_3 \ldots \lambda_{n-1}}{\mu_2\,\mu_3\,\mu_4 \ldots \mu_n}\pi_1,$$

that we obtain when considering one permanently infected individual for an SIS model with $\mu_j = \mu(j-1)$ and $\lambda_j = \lambda j(N-j)/N$, $j = 1, 2, \ldots, N$. Hence

$$\pi_k = \pi_1 \frac{\mu^{-k}}{(k-1)!} \prod_{j=1}^{k-1} \lambda_j \tag{2.2}$$

$$\pi_k = \pi_1 \frac{\mu^{-k}}{(k-1)!} (\lambda/N)^k \, (k-1)! \, (N-1)! \, / (N-k)!$$

$$= \pi_1 \frac{(\lambda/N\mu)^k}{(N-k)!} (N-1)!.$$

Denote p_k as the QSD of the number of susceptibles, then $p_k = \pi_{N-k}$. Thus

$$p_k = \pi_1 \frac{(\lambda/N\mu)^{N-k}}{k!} (N-1)!$$

and

$$\pi_1 = \left((N-1)! \sum_{j=1}^{N} (\lambda/N\mu)^{N-j}/j! \right)^{-1}$$

$$= \left((N-1)! \, (\lambda/N\mu)^N \sum_{j=1}^{N} (\lambda/N\mu)^{-j}/j! \right)^{-1}.$$

Therefore

$$p_k = \frac{(N\mu/\lambda)^k}{k! \sum_{j=1}^{N} (\lambda/N\mu)^j/j!},$$

whose limit when $N \to \infty$ provided that $N\mu/\lambda$ tends to a constant, is

$$p_k = \frac{(N\mu/\lambda)^k}{k!\,(e^{N\mu/\lambda} - 1)}, \tag{2.3}$$

a truncated Poisson random variable. Observe that if the limiting constant $N\mu/\lambda$ is large then the QSD for the number of susceptibles can be approximated with a Poisson random variable with parameter $N\rho^{-1}$. Surprisingly, this simple result was never derived in spite of the fact that Nåsell (1993) had already established that the approximations to the QSD for the infective individuals yield a normal distribution with mean $N(1-\rho^{-1})$ and variance N/ρ. This result can be obtained directly from (2.3) with $N\mu/\lambda$ large, using $\pi_{N-k} = p_k$, since then the approximation to the QSD for the susceptibles is approximately normal with mean and variance N/ρ, hence, that of the infectives is normal with mean $N(1-\rho^{-1})$ and variance N/ρ.

2.4 The approximation to the quasi-stationary distribution of the number of susceptibles for non-exponential duration of the illness state: an application of queuing theory.

An SIS epidemic process can also be seen as a queuing process with state dependent arrival rate. We can think of N servers, where a busy server corresponds to an infective individual. Individuals are served at a rate μ, and the arrival rate being

$\lambda j(N-j)/N$ when the number of busy servers is j. This analogy will be used to derive an approximation to the QSD of the number of susceptible individuals.

The constant hazard rate characteristic of the exponential distribution makes it difficult to adopt for most diseases. The idea of assuming that the probability that a person will be cured in the nexts s units of time given that s/he has been infected during a time t, is independent of t is not very realistic. In this section we derive a new result for the approximation to the QSD of SIS models when the illness state is non exponential.

From queuing theory, (see Van Hoorn, 1984) the limiting distribution of the number of busy servers with state dependent arrival rate is given by

$$\pi_k = \pi_1 \frac{(\mathrm{E}\,\mathbf{S})^k}{k!} \prod_{j=0}^{k-1} \lambda_j, \tag{2.4}$$

where E S is the expected value of the service time. Thus, (2.2) is is a particular case of (2.4) with the proviso that state 0 is never visited. Hence, the approximation to the QSD for the number of busy servers (infectives) depends on the duration of the illness state only through its first moment. The general expression for the reflecting state QSD of the number of susceptibles becomes

$$p_k = \frac{\left(\frac{N}{\lambda \mathrm{E}\,\boldsymbol{S}}\right)^k}{k!\,\left(e^{N/\lambda \mathrm{E}\,\mathbf{S}} - 1\right)}. \tag{2.5}$$

Observe that, for $N/\lambda \mathrm{E}\,\boldsymbol{S}$ large, p_k can be approximated by a Poisson distribution with parameter $N/\lambda \mathrm{E}\,\boldsymbol{S}$. Therefore, the approximation to the QSD of the

number of infectives can be approximated with a Normal distribution with mean $N(1 - 1/\lambda \mathrm{E}\, \boldsymbol{S})$ and variance $N/\lambda \mathrm{E}\, \boldsymbol{S}$. We refer to the next section for numerical evaluations.

2.5 Simulations.

In this section, several SIS epidemic models are simulated for different values of λ, keeping $N = 200$, $\mu = 1$ and $\lambda/\mu > 1$. A Gamma distribution is assumed for the duration of the illness state with three sets of parameters. Simulations were performed using MATLAB. Only the distribution of susceptibles is plotted against the approximated (2.5). Fig. 2.1 shows the distributions used for the duration of the illness state. Figs. 2.2-2.4 show the QSD (histogram) and the approximation (solid line.

The simulations were performed in MATLAB 5.0. These were implemented as follows: for each parameter set, an stochastic SIS epidemics was simulated an it was recorded the time spent on each state during a large amount of time. The distribution of the time spent on each state is ploted against the approximation (2.5). The code for the program is in the appendix under A.1.

3 The SEIS Model

3.1 Introduction.

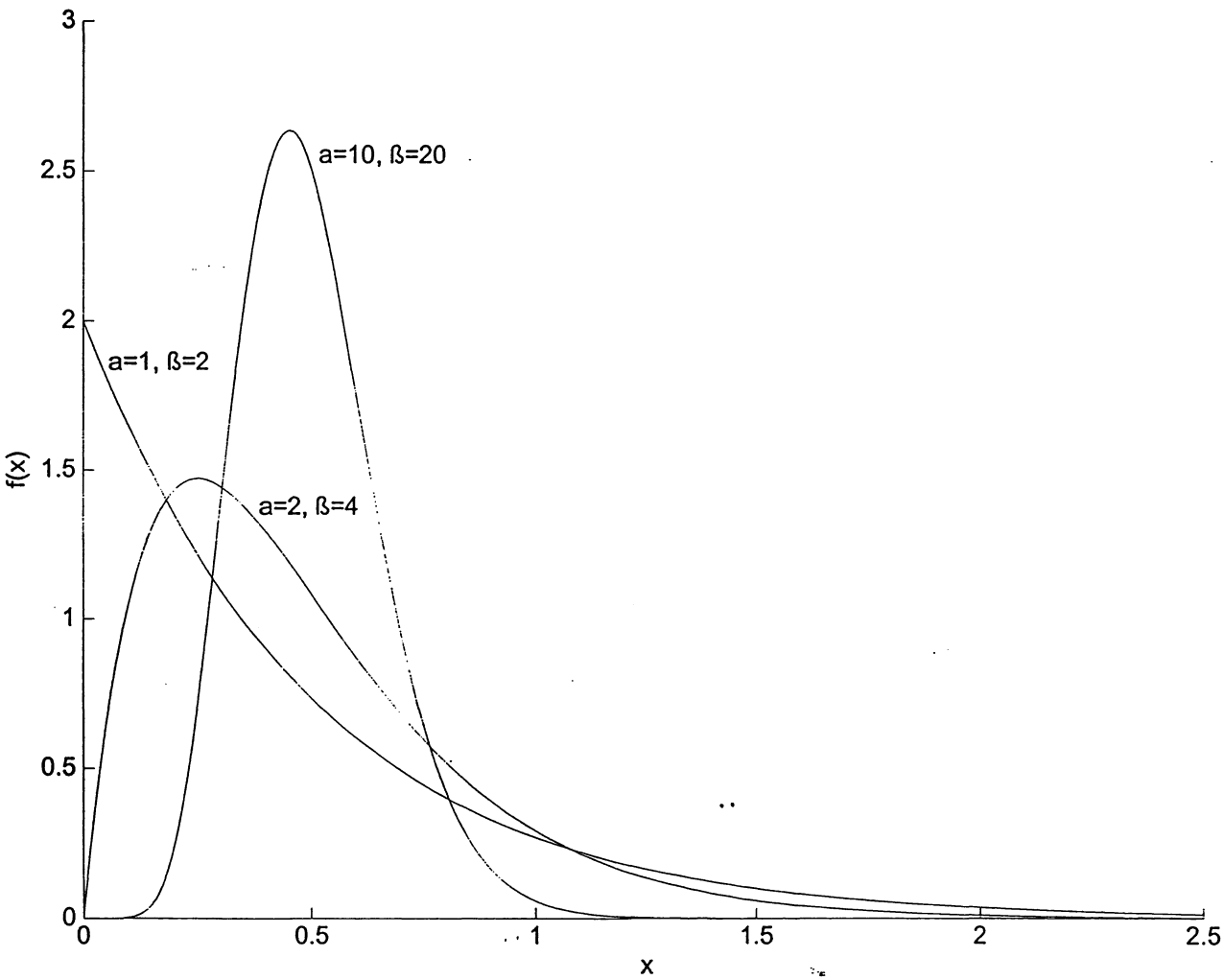

Figure 2.1 Distribution of the duration of the infectious state

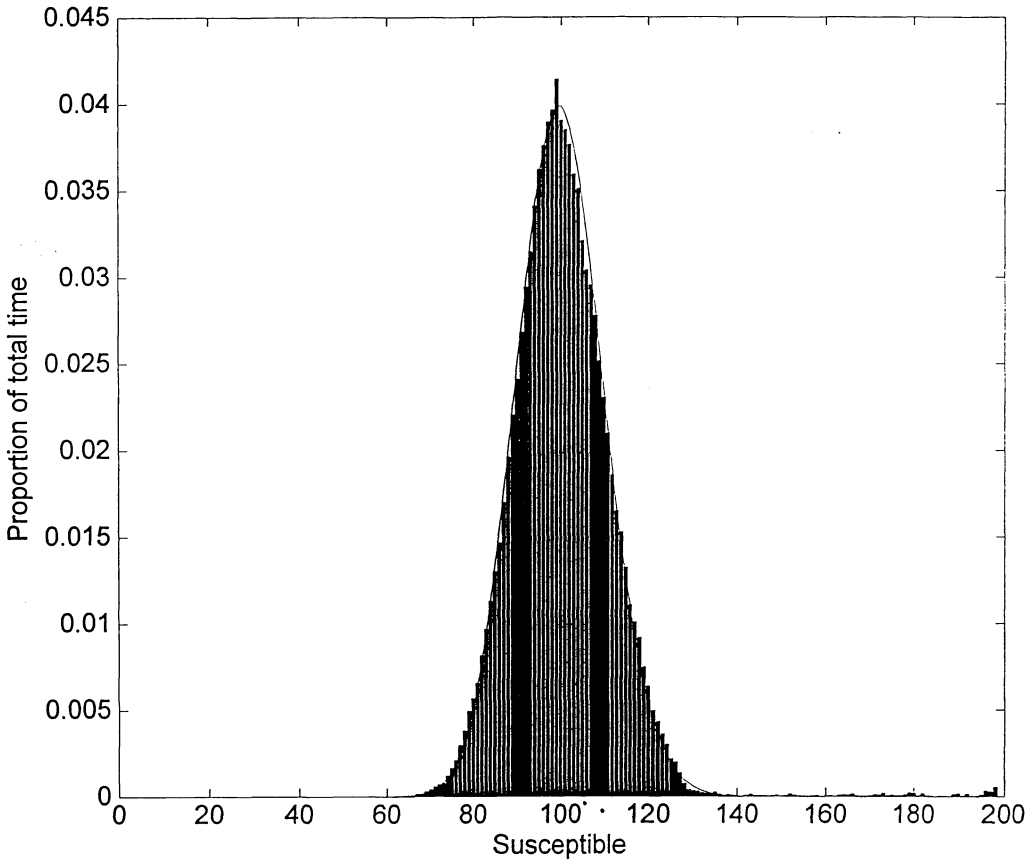

Figure 2.2 The quasistationary distribution and its approximation (solid line). $N = 200$, $\lambda = 4$, $\alpha = 1$, $\beta = 2$, Time = 500 units

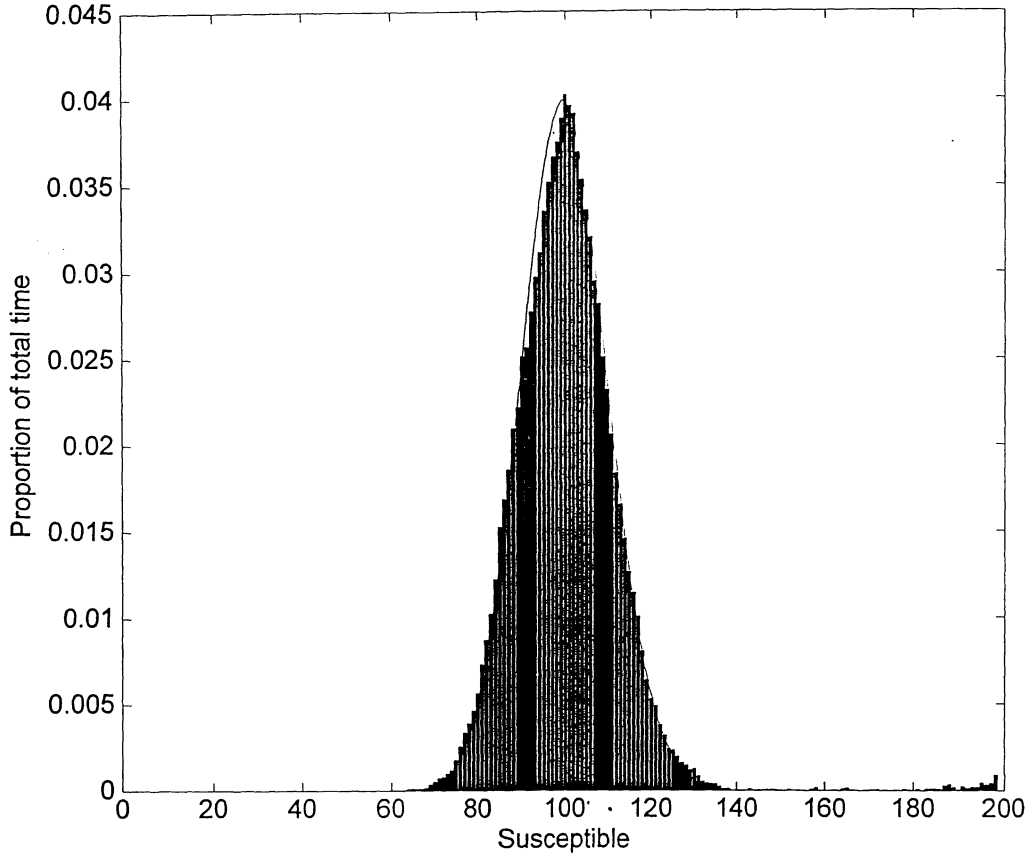

Figure 2.3 The quasistationary distribution and its approximation (solid line). $N = 200$, $\lambda = 4$, $\alpha = 2$, $\beta = 4$, Time = 500 units

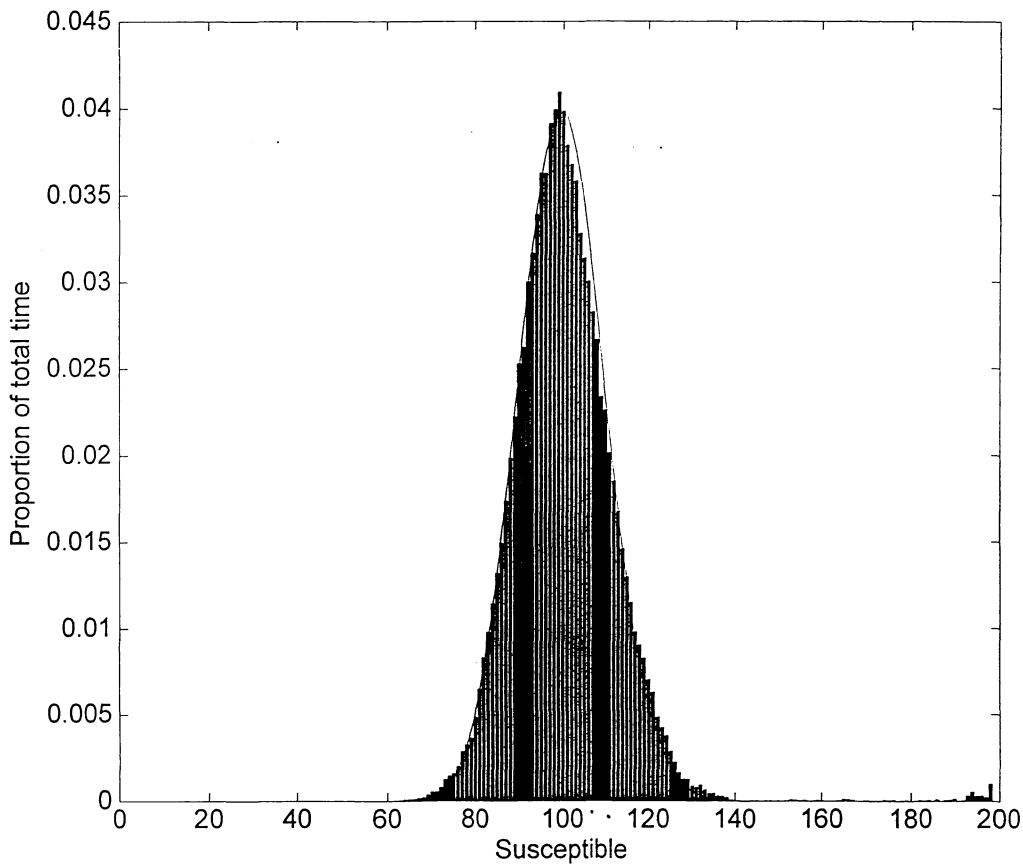

Figure 2.4 The quasistationary distribution and its approximation (solid line). $N = 200$, $\lambda = 4$, $\alpha = 10$, $\beta = 20$, Time = 500 units

A natural generalization of the SIS model is to consider additional epidemiological states. Here we consider the possibility that an infective individual undergoes a latent state before becoming infectious. That is, individuals who become infected are not able to transmit the disease for a period of time. Since infected individuals in the latent state can not transmit the disease or acquire additional infection, they play no role in the transmission of the epidemics but rather serve as buffers or reservoirs of infection. This model is refered as the SEIS model or SLIS model.

Quasi-stationary distributions for SEIS models are two-dimensional arrays, $\pi_{m,n}$, where $\pi_{m,n}$ denotes the limiting proportion of time in which there were m latent and n infective individuals conditioning in the process not being in the absorbing state. It is possible to define a QSD for the total number of infective individuals π_k where $k = m + n$. In this section it is shown how the QSD for the total infected in a population in an SEIS model can be derived from that of an SIS model. From this last result the two-dimensional QSD follows directly.

An approximation to the joint QSD of the Ross malaria model was given by Nåsell (1991) The state space of the process can be stated in terms of the number of latent and infective individuals, (E,I) as:

$$\Omega = \{(e,i);\ e+i \leq N,\ e,i \in Z^+\}$$

The following diagram explains shows the transitions between the different epidemiological states:

$$S \xrightarrow{\lambda SI/N} E \xrightarrow{\mu_1 E} I \xrightarrow{\mu_2 I} S$$

3.2 The quasi-stationary distribution of the SEIS model

Define:

$$P_{i,j;\,k,m}(s,t) = P\{E(t) = k, I(t) = m \,|\, E(s) = i, I(s) = j\},$$

$$\{k,m\}, \{i,j\}, \in \Omega,\ 0 \leq s \leq t$$

where $E(t)$ and $I(t)$ are random variables tha denote the number of latent and infective individuals at time t, respectivelly. The instantaneous transition rates are given by

$$P_{k,m;k+1,m}(t, t+\delta) = \lambda\, \delta\, m(N-k-m)/N + o(\delta),$$

$$P_{k,m;k-1,m+1}(t, t+\delta) = \mu_1\, \delta\, k + o(\delta),$$

$$P_{k,m;k,m-1}(t, t+\delta) = \mu_2\, \delta\, m + o(\delta),$$

while all other events are assumed to occur with probability $o(\delta)$. In section 3.2.1 an approximation to the QSD of the total number of infected people (latent + infective)

is derived. In section 3.2.2 the joint QSD distribution of the latent and infective is analyzed.

3.2.1 The quasi-stationary distribution of the total number of infected in the SEIS model

We introduce the random variable $I^*(t) = E(t) + I(t)$ which denotes the total number of infected individuals at time t. Define also:

$$P^*_{j,k}(s,t) = P\{I^*(t) = k \,|\, I^*(s) = j\},\ j,k \in [0,N];\ 0 \leq s \leq t \qquad (2.6)$$

and call p^*_k the $k-th$ element of the QSD of this process. To derive the approximation to the quasi-stationary distribution, it sufices to start from the instantaneous transition rates when $t \to \infty$ in (2.6), and considering that j in (2.6) is k, $k-1$ or $k+1$.

Chose an arbitrary but fixed time t. From renewal theory (Cox 1962, pp. 80-86) when $t \to \infty$, the probability that an individual is the infective state given that he is infected (latent or infective) is

$$\mu_2^{-1}\left(\mu_1^{-1} + \mu_2^{-1}\right)^{-1} \equiv \theta_{\mathrm{I}},$$

and conditioning in having exactly k infected, the number of infective individuals follows a Binomial distribution with parameters k and θ_{I}. That is

$$\lim_{t\to\infty} P(I(t)=j|\, I^*(t)=k) = \binom{k}{j}\theta_I^j(1-\theta_I)^{k-j}. \tag{2.7}$$

We now proceed to prove the main result of this section. Conditioning in the process not being in the absorbing state, when $t \to \infty$ and $\delta \to 0$ the probability of a new infection in $(t, t+\delta)$ is

$$\lim_{\substack{t\to\infty \\ \delta\to 0}} P^*_{k+1,k}(t+\delta, t) =$$

$$\lim_{\substack{t\to\infty \\ \delta\to 0}} P\{I^*(t+\delta) = k+1 \,\big|\, I^*(t) = k\},\ k \in \Omega^*];\ 0 \le s \le t$$

where $\Omega^* = \{1, 2, 3, \ldots N\}$. Applying the total probability law, we can rewrite the last expression as:

$$\lim_{\substack{t\to\infty \\ \delta\to 0}} \sum_{j=0}^{k} P\{(I^*(t+\delta) = k+1,\ I(t) = j) \,\big|\, I^*(t) = k\},$$

$$= \lim_{\substack{t\to\infty \\ \delta\to 0}} \sum_{j=0}^{k} \frac{P\{I(t+\delta) = k+1,\ I(t) = j,\ I^*(t) = k\}}{P\{\, I^*(t) = k\}}.$$

Using $P\{\, I^*(t) = k\} = p_k^*$ we can rewrite the last expression as

$$\lim_{\substack{t\to\infty \\ \delta\to 0}} (p_k^*)^{-1} \sum_{j=0}^{k} P\{(I^*(t+\delta) = k+1,\ I(t) = j), I^*(t) = k\}. \tag{2.8}$$

The term inside the sum is:

$$p_k^* \sum_{j=0}^{k} \Big(P\{I(t)=j \,|\, I^*(t)=k\} P\{I(t+\delta)=k+1 \,|\, (I^*(t)=k \cap I(t)=j)\Big).$$

thus (2.8) simplifies to

$$\lim_{\substack{t\to\infty \\ \delta\to 0}} \sum_{j=0}^{k} \Big(P\{I(t)=j \,|\, I^*(t)=k\} P\{I(t+\delta)=k+1 \,|\, (I^*(t)=k \cap I(t)=j)\Big)$$

$$= \lim_{t\to\infty} \sum_{j=0}^{k} P(I(t)=j \,|\, I^*(t)=k)\,(\lambda\,\delta\,j\,(N-k)/N + o(\delta)),$$

then using result (2.7) , that is that $\lim_{t\to\infty} P(I(t)=j|I^*(t)=k)$ is Binomial(k,θ_{I}), then (2.8) simplifies to

$$\lambda\,\delta\,\frac{N-k}{N} \sum_{j=0}^{k} j \binom{k}{j} \theta_{\mathrm{I}}^{j} (1-\theta_{\mathrm{I}})^{k-j} + o(\delta).$$

$$= \lambda\theta_{\mathrm{I}}\,\delta\,k\,\frac{N-k}{N} + o(\delta)$$

in conclusion, we have that

$$\lim_{\substack{t\to\infty \\ \delta\to 0}} P\{I^*(t+\delta) = k+1 \,\big|\, I^*(t) = k\} = \lambda\,\theta_I\,\delta\,(N-k)/N + o(\delta) \qquad (2.9)$$

Similarly, an analogous expression for $\lim_{\substack{t\to\infty \\ \delta\to 0}} P^*_{k-1,k}(t+\delta, t)$ can be derived explicitely, since

$$\lim_{\substack{t\to\infty \\ \delta\to 0}} P^*_{k-1,k}(t+\delta, t) =$$

$$\lim_{\substack{t\to\infty \\ \delta\to 0}} P\{I^*(t+\delta) = k-1 \,\big|\, I^*(t) = k\},\ k \in \Omega^*];\ 0 \le s \le t$$

Then via the law of the total probability the last expression becomes

$$= \lim_{\substack{t\to\infty \\ \delta\to 0}} \sum_{j=0}^{k} P\{(I^*(t+\delta) = k-1 \cap I(t) = j) \,\big|\, I^*(t) = k\},$$

$$= \lim_{\substack{t\to\infty \\ \delta\to 0}} \sum_{j=0}^{k} \frac{P\{I(t+\delta) = k-1 \cap I(t) = j \cap I^*(t) = k\}}{P\{\, I^*(t) = k\}}. \qquad (2.10)$$

Analogously to (2.8), we can rewrite the term inside the sum as:

$$p_k^* \sum_{j=0}^{k} \left(P\{I(t) = j \,|\, I^*(t) = k\} P\{I(t+\delta) = k-1 \,|\, (I^*(t) = k \cap I(t) = j)\right)$$

the term outside the sumation cancels with the denominator in (2.10). After taking limites, the term inside the sum reduces to

$$\sum_{j=0}^{k} P(I(t) = j \mid I^*(t) = k) \;\; \mu_2 \, \delta \, j + o(\delta)$$

$$= \mu_2 \, \delta \sum_{j=0}^{k} j \; P(I(t) = j \mid I^*(t) = k). + o(\delta).$$

Using again the result (2.7) we finally have

$$\lim_{\substack{t \to \infty \\ \delta \to 0}} P\{I^*(t+\delta) = k-1 \,|\, I^*(t) = k\} = \mu_2 \, \delta \, \theta_I + o(\delta). \qquad (2.11)$$

Equations (2.9) and (2.11) are formally equivalent to those given by (2.1) with $\lambda \, \theta_I$ and $\mu_2 \, \theta_I$ replacing λ and μ respectively. Therefore, an approximation to the QSD of the total number of susceptible individuals in an SEIS model can be obtained directly from that of an SIS model (2.3), which is given by a truncated Poisson distribution with parameter $N\mu_2/\lambda$:

$$p_k^* = \frac{(N\mu_2/\lambda)^k}{k\,!\,(e^{N\mu_2/\lambda} - 1)} \tag{2.12}$$

In Section 2.4 it was found that the QSD for the number of infective individuals (busy servers) in an SIS epidemics model depends on the duration of the infectious period (service time)only through the first moment. Since an SEIS epidemic model can be seen as a queuing system with two phases on each server, it is natural to expect the same behavior in this case. Note that the infection rate is $\lambda\ \theta_{\mathrm{I}}$ and $\mathbf{E}\ \mathrm{S}$, the mean duration in the system is $\mu_1^{-1} + \mu_2^{-1}$.

According to (2.5), the parameter of the Poisson distribution for the number of susceptibles becomes

$$N/(\lambda\ \theta_{\mathrm{I}}\ \mathbf{E}\ \mathrm{S}) = N\Big/\big(\lambda\ \theta_{\mathrm{I}}(\mu_1^{-1} + \mu_2^{-1})\big).$$

Since $\theta_{\mathrm{I}} = \mu_2^{-1}\,(\mu_1^{-1} + \mu_2^{-1})^{-1}$, then the mean number of infected becomes $N\mu_2/\lambda$, as expected. Thus, the joint QSD has its mean at

$$(E, I) = \big(N\mu_2(1 - \theta_{\mathrm{I}})/\lambda,\ N\mu_2\theta_{\mathrm{I}}/\lambda\big) \tag{2.13}$$

It is important to observe the lack of dependence of the above result on higher moments of the duration of the latent and infectious period.

3.2.2 The marginal joint quasi-stationary distribution of the number of latent and infective individuals in the SEIS model

The QSD joint distribution for the number of latent and infective can be derived from expression (2,12). When $N\mu_2/\lambda$ is large the number of susceptibles is given approximately by a Poisson distribution with parameter $N\mu_2/\lambda$. Under the assumption that $N\mu_2/\lambda$ is large we derive an approximation to $p_{m,n}$, the joint QSD for the number of latent and infective individuals respectivelly.

The joint distribution is defined as

$$p_{m,n} = \lim_{t\to\infty} P\{E(t) = m, I(t) = n\},$$

which can be rewritten as

$$p_{m,n} = \lim_{t\to\infty} P\{E(t) = m \,|\, E(t) + I(t) = m + n\}\; P\{E(t) + I(t) = m + n\}$$

$$= \lim_{t\to\infty} P\{E(t) = m \,\big|\, I^*(t) = m + n\}\; P\{I^*(t) = m + n\}$$

$$= \lim_{t\to\infty} P\{E(t) = m \,|\, I^*(t) = m + n\}\, p^*_{N-m-n}$$

with p^*_{N-m-n} given in (2.12). Using (2.7) we conclude that

$$p_{m,n} = p^*_{N-m-n} \binom{m+n}{m} (1-\theta_{\mathrm{I}})^m\, \theta_{\mathrm{I}}^n.$$

The computation of the marginal QSD of the number of latent and infectives is straigthforward. Define the marginal QSD's for the number of latent and infectives by

$$\alpha_m = \lim_{t \to \infty} P(E(t) = m)$$

and

$$\beta_n = \lim_{t \to \infty} P(E(t) = n),$$

thus

$$\alpha_m = \sum_{k=m}^{N} P(E(t) = m \,|\, I^*(t) = k) P(I^*(t) = k)$$

$$= p^*_{N-k} \sum_{k=m}^{N} \binom{k}{m} (1 - \theta_{\mathrm{I}})^m \theta_{\mathrm{I}}^{k-m}$$

and using a similar argument

$$\beta_n = p^*_{N-k} \sum_{k=n}^{N} \binom{k}{n} (1 - \theta_{\mathrm{I}})^{k-n} \theta_{\mathrm{I}}^n$$

These approximations are evaluated in the following section.

3.2.3 Simulations.

In this section, several SEIS epidemic models are simulated for different values of λ, μ_1 and μ_2, with $N = 100$. Only the case of an exponential distribution is evaluated. Both observed and theoretical distributions are plotted for a) the number of susceptibles and b) the joint (infected, latent) distribution. A contour diagram proves to be very useful for comparing the theoretical and observed joint distributions. For every set of parameters, a simulation of an SEIS epidemic model was run for a long time, and the proportion of time spent on each state was recorded. The MATLAB code is in the appendix.

3.3 The expected time elapsed between two infections of a particular individual.

Queuing theory is useful if one wishes to perform calculation of some quantities in epidemic processes. Mollison (1995) found that for epidemic process in equilibrium the proportion of the population π_i on a given state $i$is proportional to the mean time τ_i that a typical individual spends in that state, that is, he found that

$$\pi_i = \tau_i / L, \tag{2.14}$$

where L is the mean life time of an individual. Mollison called this the "microcosmos principle". Now, suppose that we have a situation in which there are N servers (one for each member of the population), an arrival rate $f(\beta)$ and a service rate μ, and that we are interested in the proportion of busy servers. If service means being infected,

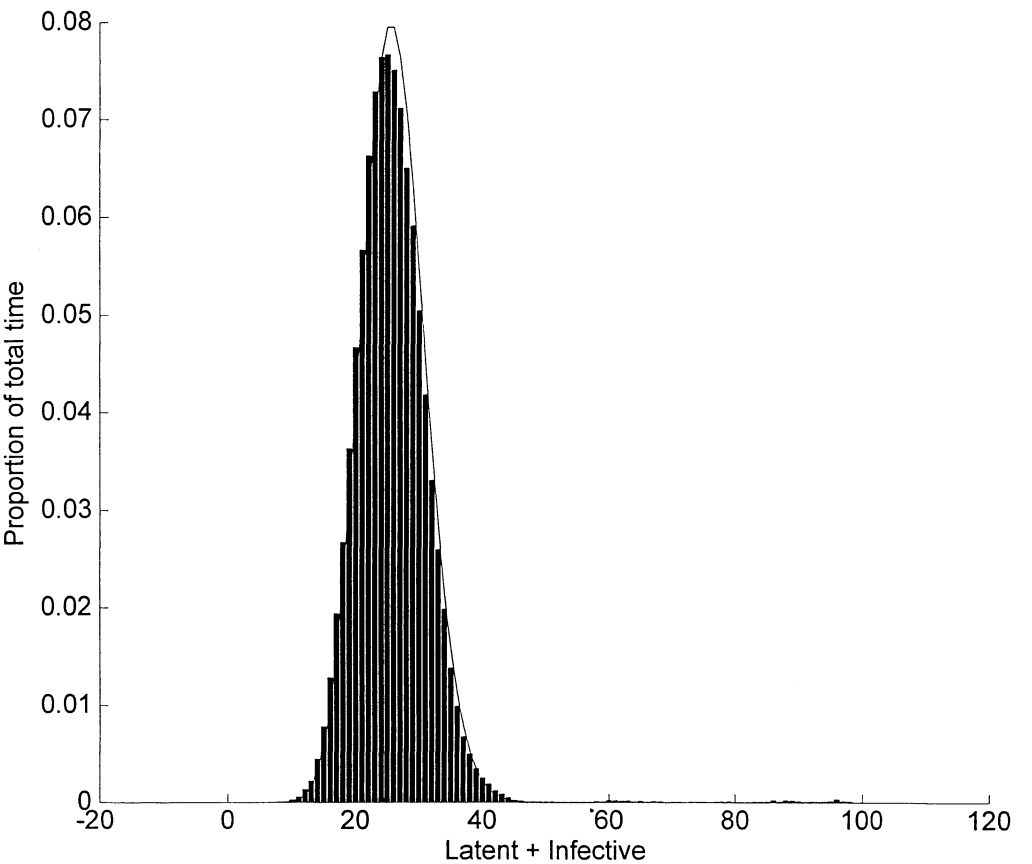

Figure 2.5 The quasistationary distribution to the total number of infected and its approximation (solid line). $N = 100$, $\lambda = 4$, $\mu_1 = 0.5$, $\mu_2 = 1$ Time = 2000 units

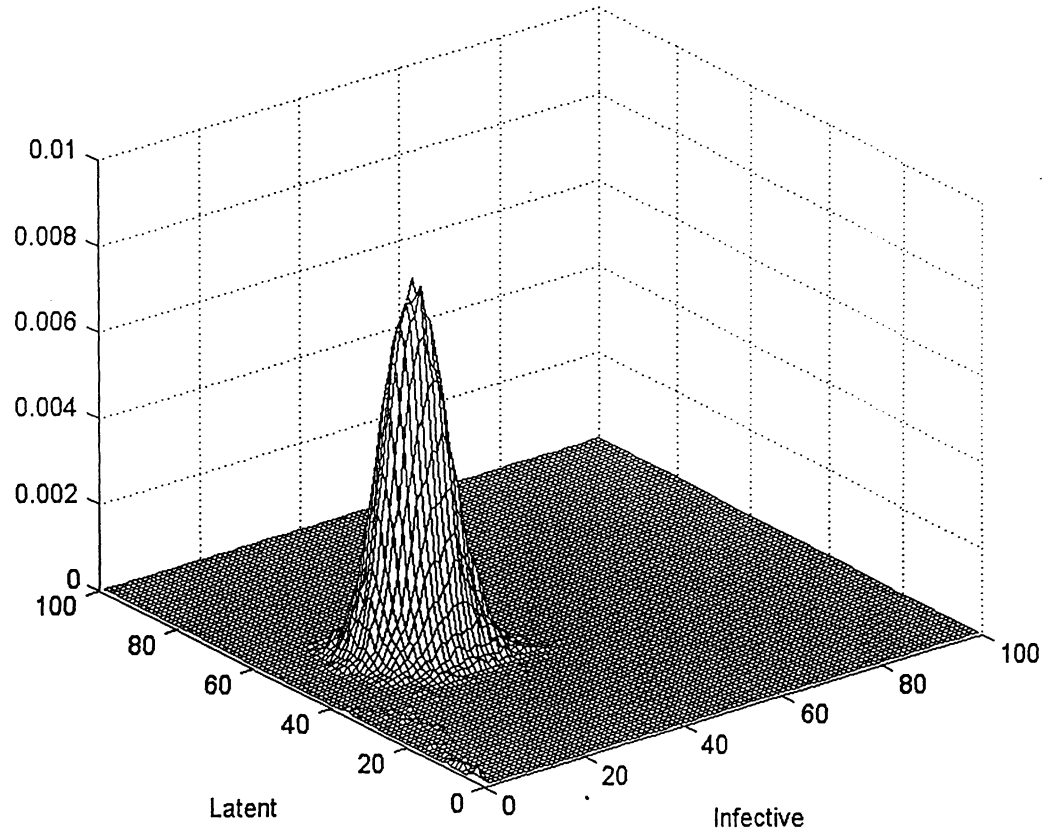

Figure 2.6 The joint quasistationary distribution of infected and latent.
$N = 100$, $\lambda = 4$, $\mu_1 = 0.5$, $\mu_2 = 1$ Time = 2000 units

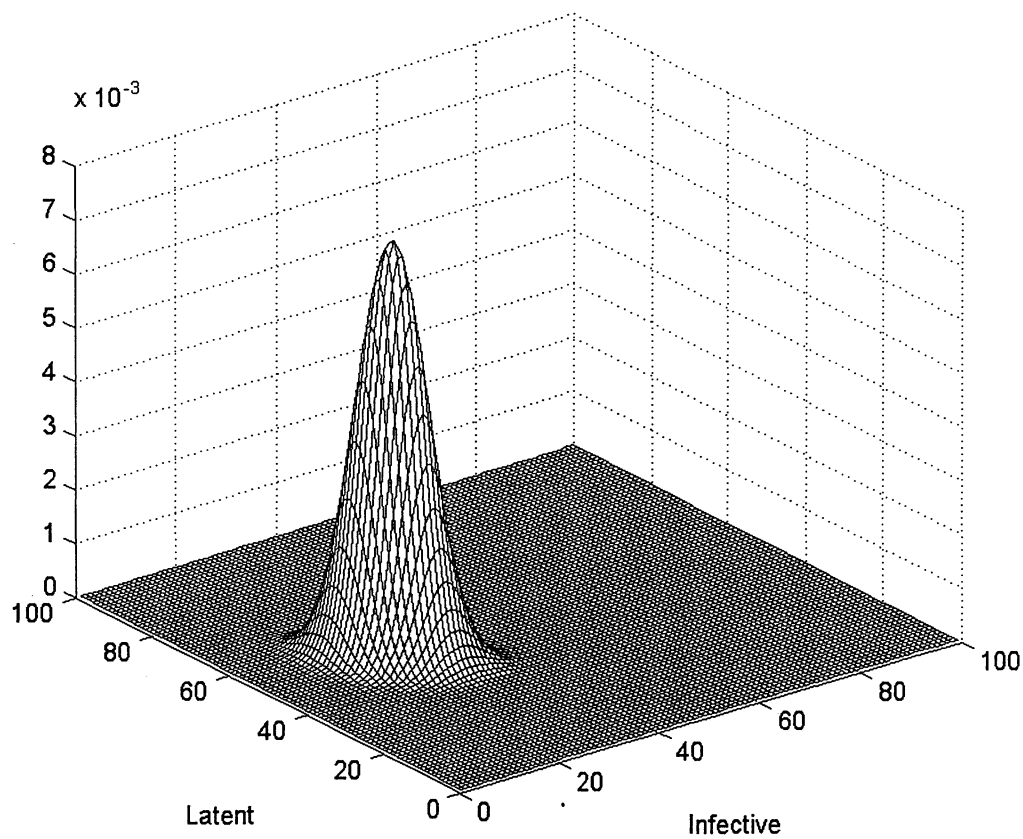

Figure 2.7 The approximation to the joint quasistationary distribution of infected and latent. $N = 100$, $\lambda = 4$, $\mu_1 = 0.5$, $\mu_2 = 1$

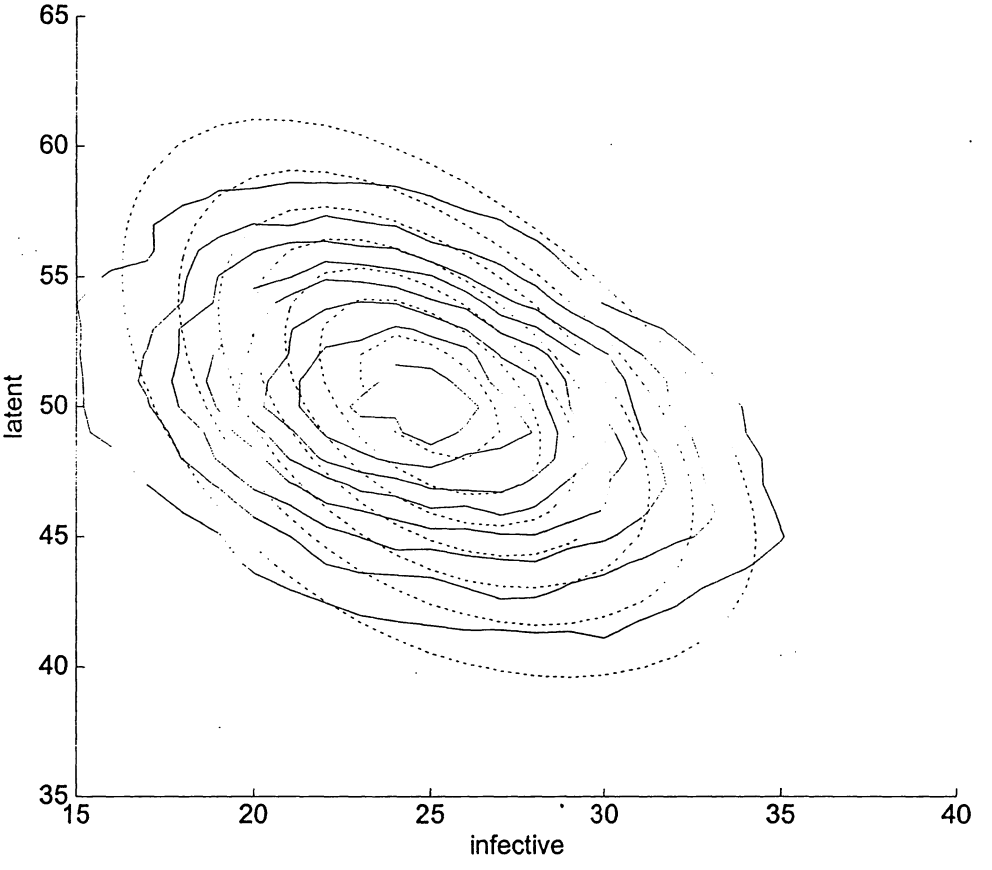

Figure 2.8 Contour diagram of the joint QSD (solid line) and its approximation (dotted line) $N = 100$, $\lambda = 4$, $\mu_1 = 0.5$, $\mu_2 = 1$ T = 2000 units

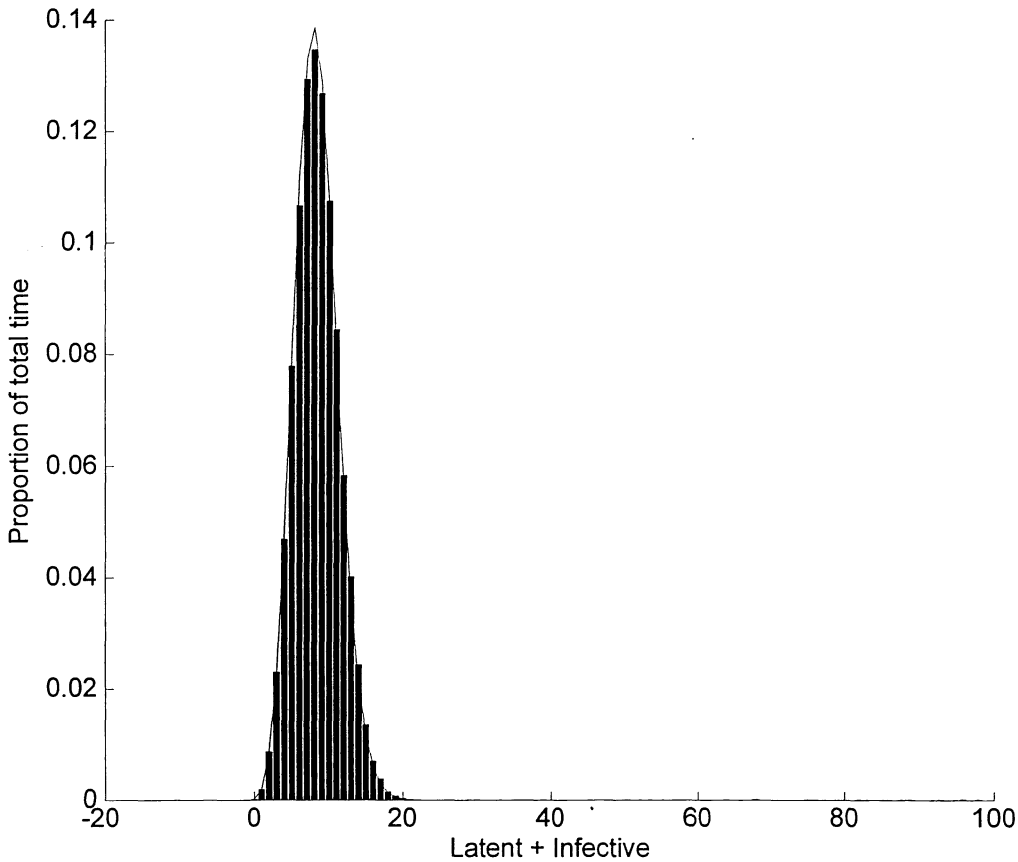

Figure 2.9 The quasistationary distribution to the total number of infected and its approximation (solid line). $N = 100$, $\lambda = 6$, $\mu_1 = 1$, $\mu_2 = 0.5$ Time = 2000 units

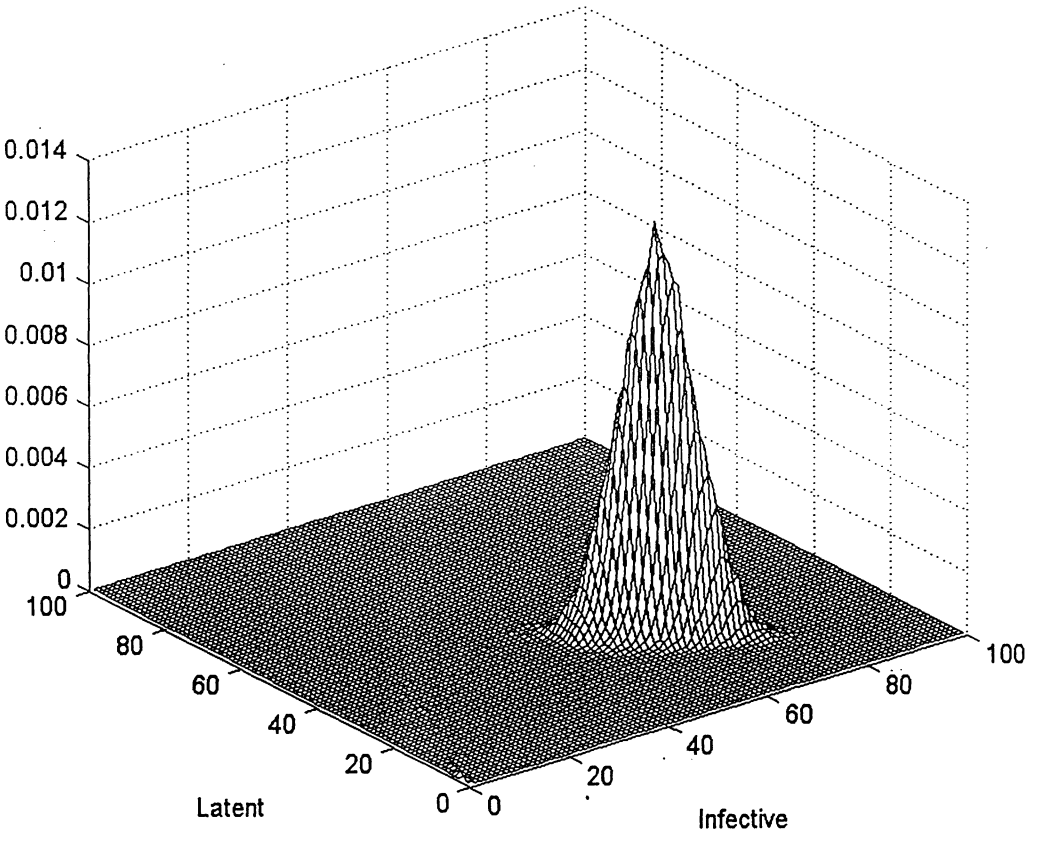

Figure 2.10 The joint quasistationary distribution of infected and latent.
$N = 100$, $\lambda = 6$, $\mu_1 = 1$, $\mu_2 = 0.5$ Time = 2000 units

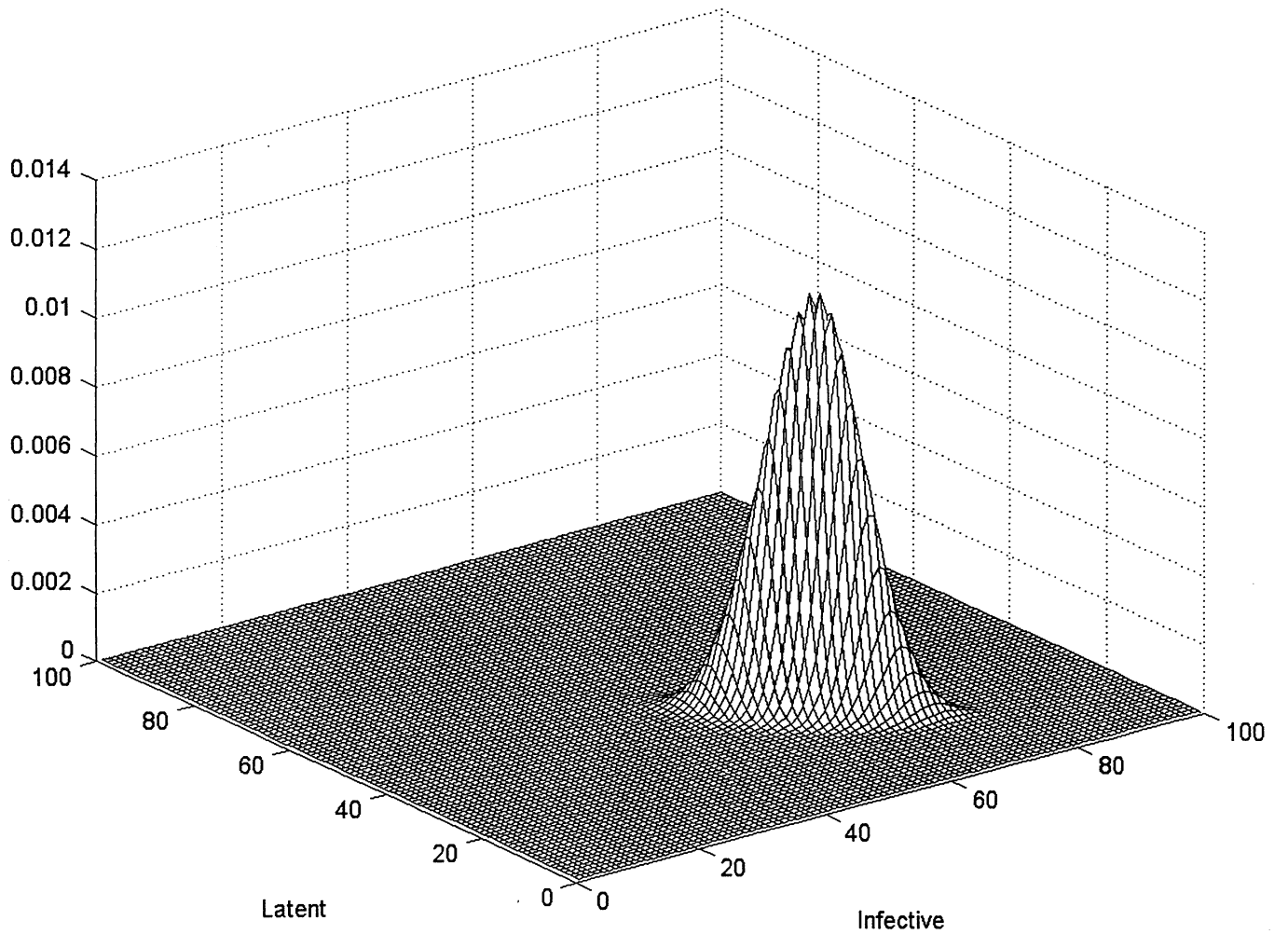

Figure 2.11 The approximation to the joint quasistationary distribution of infected and latent. $N = 100$, $\lambda = 6$, $\mu_1 = 1$, $\mu_2 = 0.5$

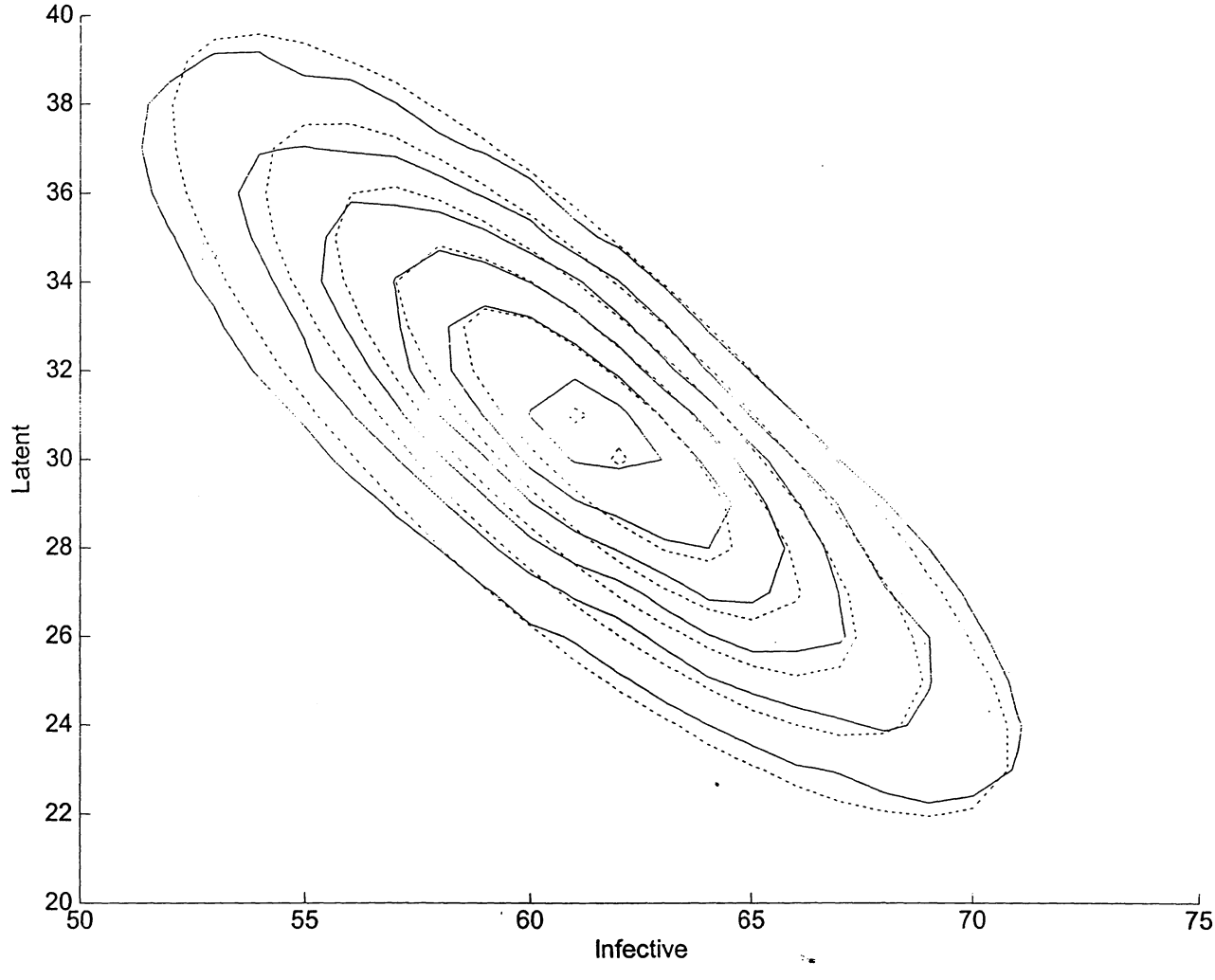

Figure 2.12 Contour diagram of the joint QSD (solid line) and its approximation (dotted line) $N = 100$, $\lambda = 6$, $\mu_1 = 1$, $\mu_2 = 0.5$ T = 2000 units

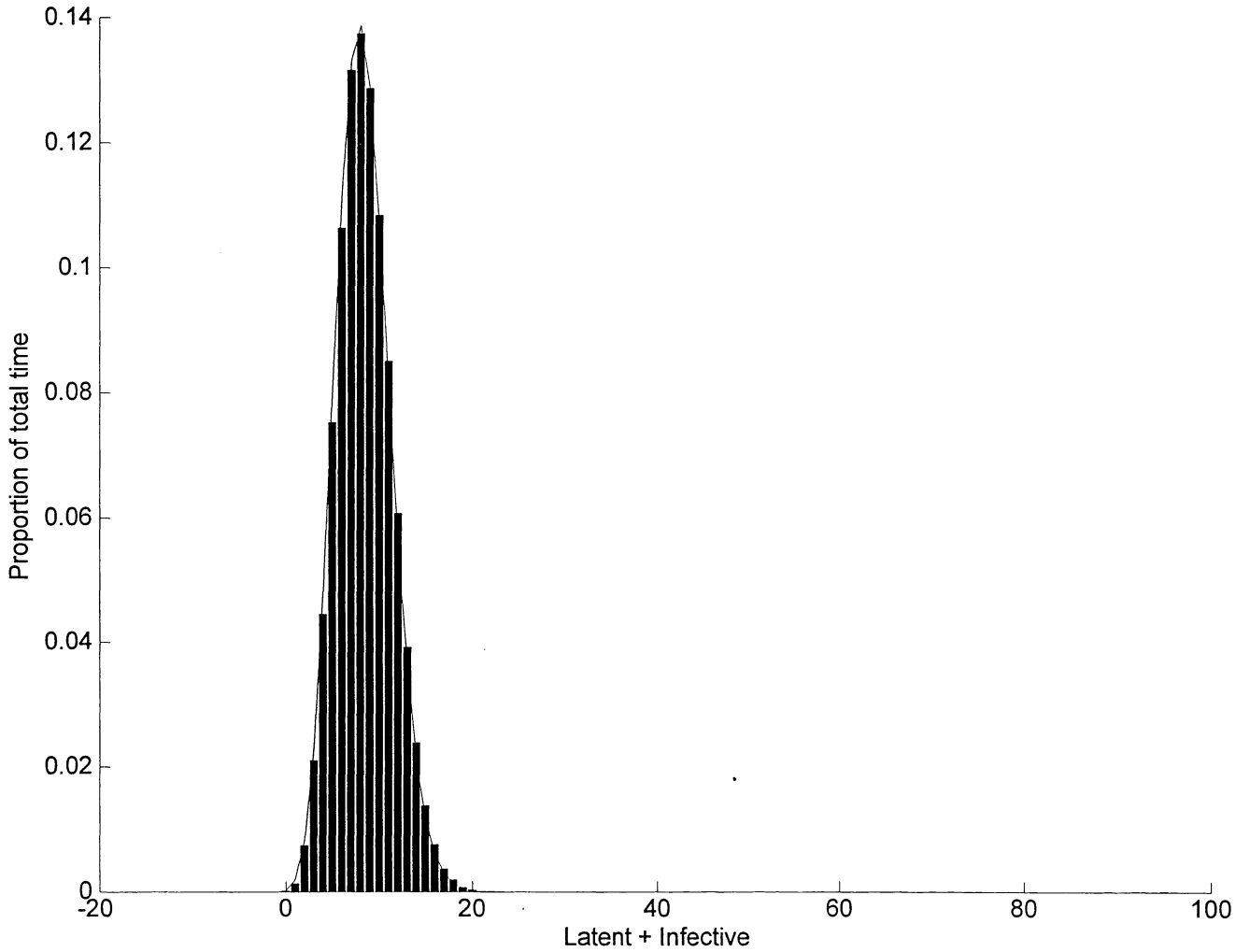

Figure 2.13 The quasistationary distribution to the total number of infected and its approximation (solid line). $N = 100$, $\lambda = 6$, $\mu_1 = 3$, $\mu_2 = 0.5$ Time = 2000 units.

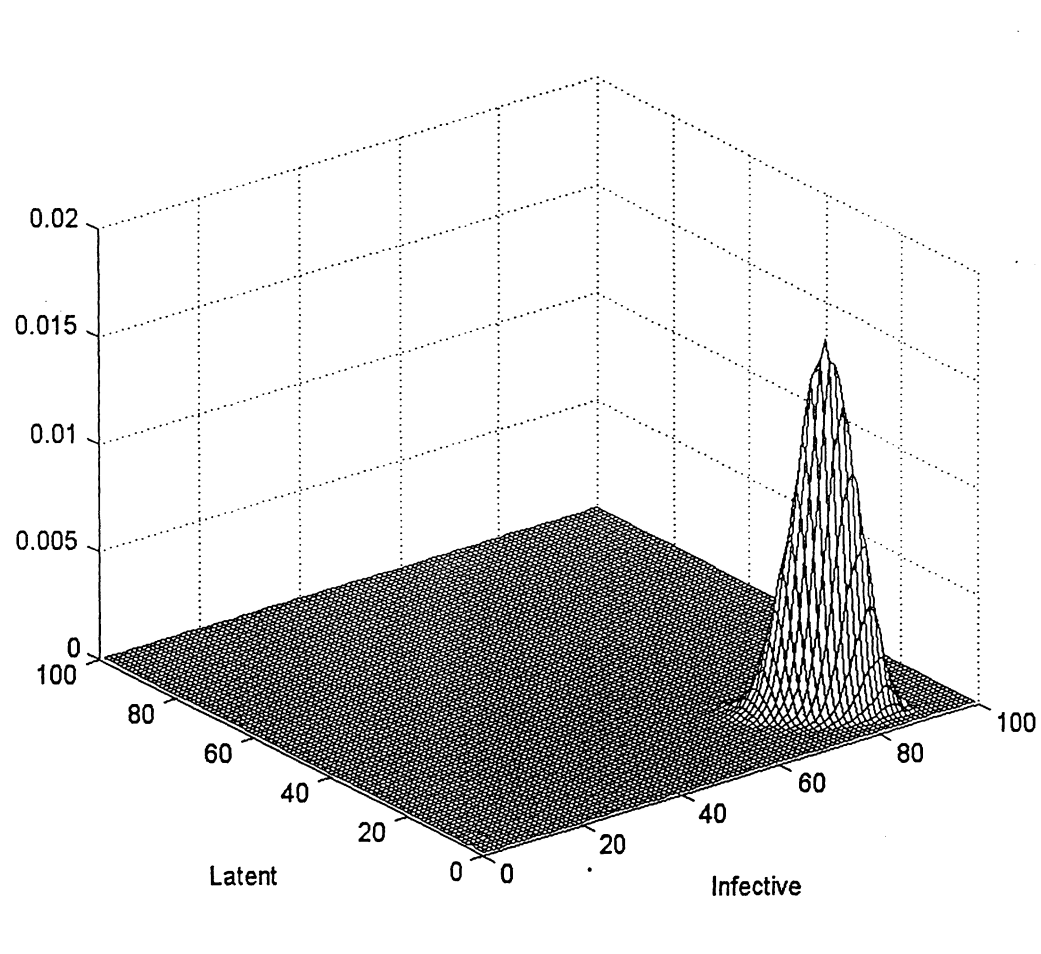

Figure 2.14 The joint quasistationary distribution of infected and latent.
$N = 100$, $\lambda = 6$, $\mu_1 = 3$, $\mu_2 = 0.5$ Time = 2000 units

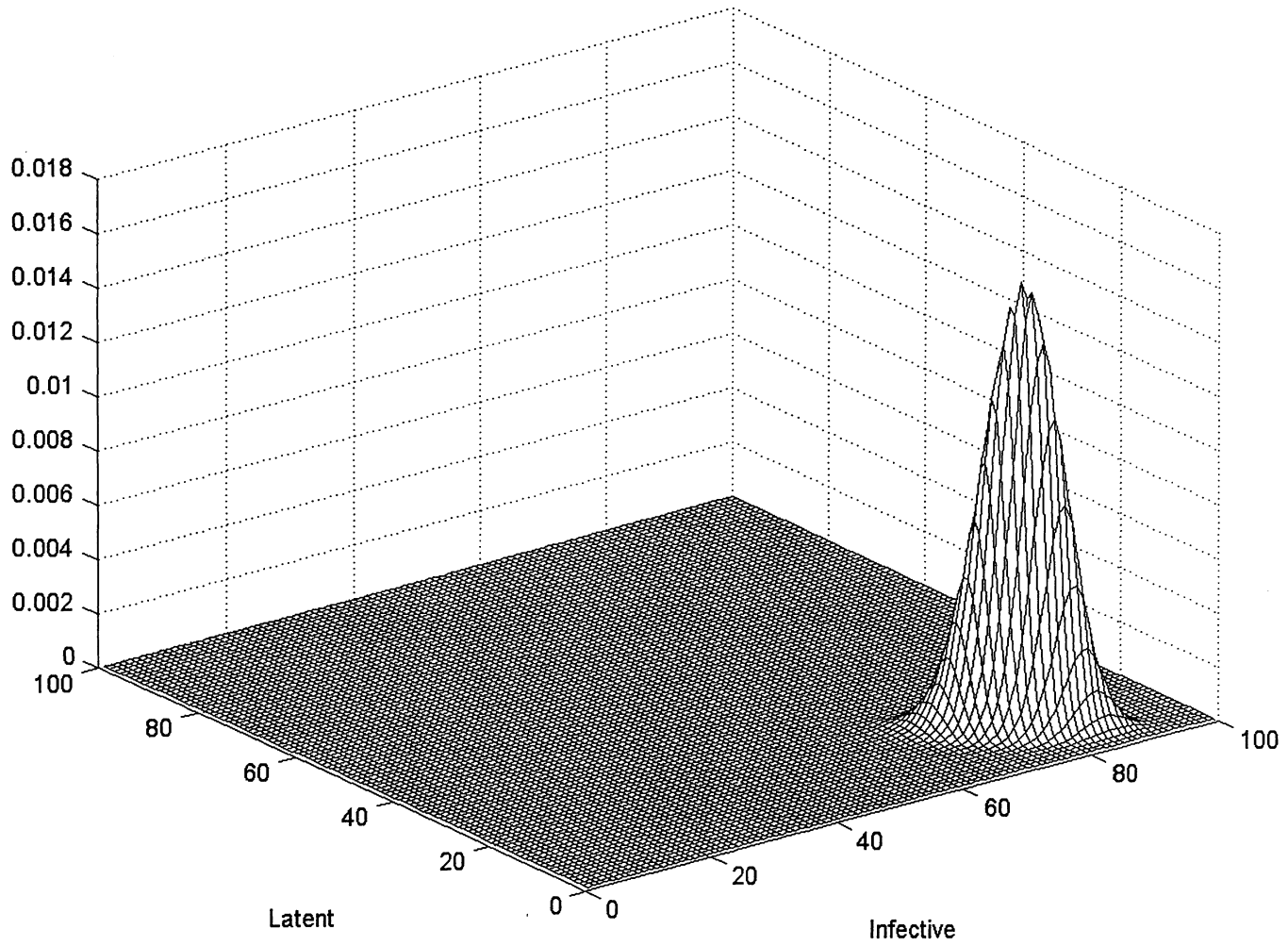

Figure 2.15 The approximation to the joint quasistationary distribution of infected and latent. $N = 100$, $\lambda = 6$, $\mu_1 = 3$, $\mu_2 = 0.5$

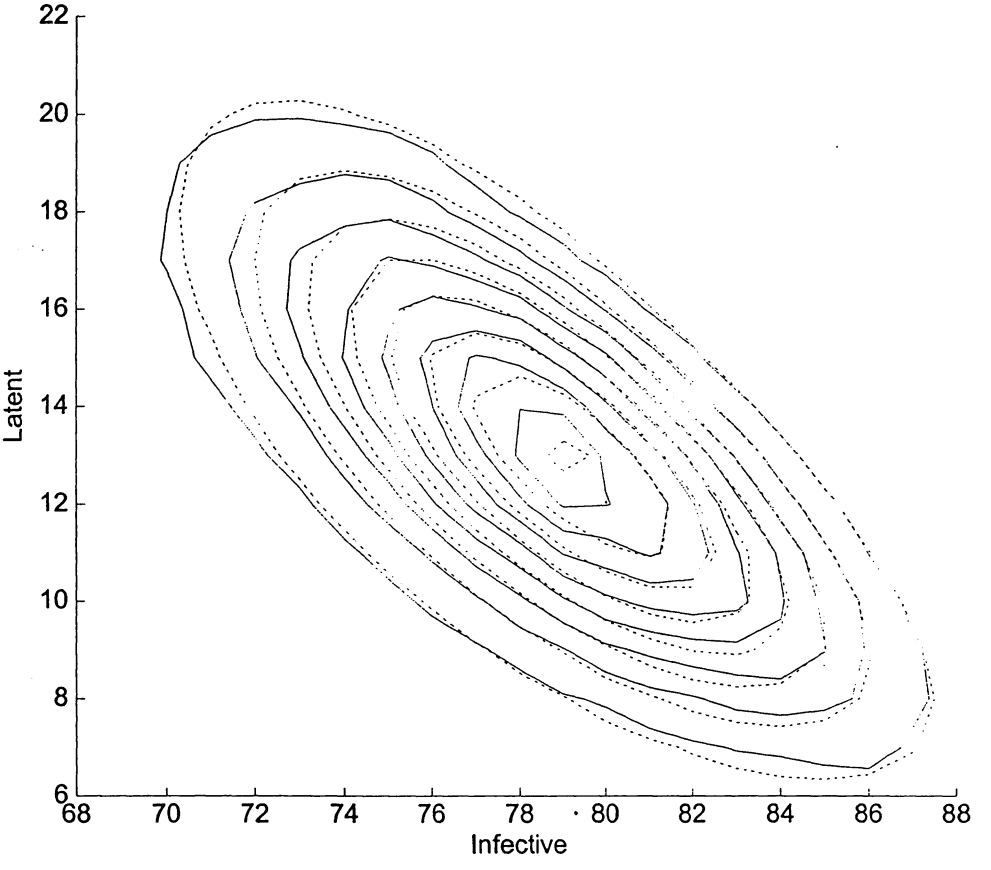

Figure 2.16 Contour diagram of the joint QSD (solid line) and its approximation (dotted line) $N = 100$, $\lambda = 6$, $\mu_1 = 3$, $\mu_2 = 0.5$ T = 2000 units

then τ_i in (2.14) is μ^{-1}. Let the mean span life of an individual be L, then deaths occur at a rate NL^{-1}. That is, individuals enter the infectious state at rate NL^{-1} which we know is $f(\beta)$. Therefore $L^{-1} = f(\beta)/N$ and (2.14) can be rewritten as:

$$\pi_i = \mu^{-1} f(\beta)/N,$$

or as

$$N\pi_i = \mu^{-1} f(\beta).$$

Or in other words

Average number of busy servers = mean service time $\times$ arrival rate

which is "Little's law", perhaps the simplest and best known of the equalities in Queuing Theory. This equality comes in turn from the fact that when in equilibria both infections (arrivals) and recoveries (services) must occur at the same rate.

Thus, at equilibrium the probability that a particular individual (server) is infective (busy) at a particular time is also π_i. From (2.5) $\pi_i = 1 - \mu/\lambda$. Since in equilibrium the rate at which a particular servers becomes busy is

$$\lambda\pi_i(1 - \pi_i) = \mu(1 - \mu/\lambda)$$

then the interarrival time between infections of a particular individual is given by

$$\frac{\lambda}{\mu(\lambda - \mu)}.$$

Notice that λ/μ, the expected number of secondary cases of infection originated by an infection individual in a population of susceptibles (R_0 in

deterministic epidemics models) corresponds to the *server utilization* in queuing systems. The server utilization is the long run proportion of time a server is busy.

4 Conclusions

The simulations show that the approximation is accurate in both SIS and SEIS epidemic models, in agreement with (2.12) for the infected and (2.13) for the joint distribution. Since these are limit distributions, it is important to run the simulations for a large time to obtain appropriate sample from the targetted distributions. It can be observed in Fig 2.6 a small path starting close to the origin that shows the evolution of the process towards the equilibria.

It is important to stress that the distribution of the QSD of the latent plus infective depends only on the infection rate λ and on the recovery rate from the infectious state μ_2. This can be seen in Figs. 2.9 and 2.13, that differ only in the parameter μ_1. It is intuitive that this holds for epidemic models of the form S-E_1-E_2-$\cdots$$E_k$-$I$. In addition, for these models, the joint and marginal distribution depends on the latent states only through the mean in the series of latent states.

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